SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _	· · · · · · · · · · · · · · · · · · ·	Examiner # :	Date:
Art Unit:	Phone Number 30	Serial Number:	•
Mail Box and Bldg/Room	Location:	Results Format Preferred (circle):	PAPER DISK E-MA
If more than one search	is submitted, please	prioritize searches in order of ne	ed.
Please provide a detailed stater Include the elected species or s	nent of the search topic, and tructures, keywords, synony any terms that may have a	describe as specifically as possible the sub orns, acronyms, and registry numbers, and c special meaning. Give examples or relevan	ject matter to be searched.
Title of Invention:			
Inventors (please provide ful	names):		
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Earliest Priority Filing Da			
For Sequence Searches Only lappropriate serial number.	Please include all pertinent inf	ormation (parent, child, divisional, or issued pa	stent numbers) along with the
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STAFF USE ONLY	Type of Search	Vendors and cost whe	re applicable
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Searcher Phone #:	AA Sequence (#)_	Dialog	
Searcher Location:	Structure (#)	Questel/Orbit	,
Date Searcher Picked Up:		Dr.Link	
Date Completed: 4/10	Litigation	Lexis/Nexis	
earcher Prep & Review Time:	Fulltext	Sequence Systems	
Rerical Prep Time:	Patent Family	WWW/Internet	

PTO-1590 (8-01)

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Strausberg R.;
Submitted (MAY-2001)
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Q26565 schistosoma	Q26565	ហ	161		12
Q9m530 euphorbia e	Q9M530	10	160		12
canis 1	Q9MZD3	თ	156		12
065191 fucus disti	065191	10	112	5.8	12
homo	Q9BVG1	4.	105		12
Q13427 homo sapien	Q13427	4	754		13
Ç,	055035	11	752	6.2	13
5	Q96DG9	4	357	6.2	13
Q9ly53 arabidopsis	Q9LY53	10	234		13
Q9hfu3 magnaporthe	Q9HFU3	w	215	6.2	13
Q26994 toxoplasma	Q26994	G	179		13
Q96417 digitalis l	Q96417	10	172	6.2	13
Q9hfu2 magnaporthe	Q9HFU2	w	165		13
Q98ue5 xenopus lae	Q98UE5	13	104		13
Q9qwd4 rattus sp.	Q9QWD4	1	87		13
Q26551 schistosoma	Q26551	5	213	-	14
O65104 chlamydomon	065104	10	172	6.7	14
	Q27716	տ	210		15
Q9u6u5 plasmodium	Q906US	տ	210		15
Q9d868 mus musculu	Q9D868	11	188	7.2	15
Q9v9b9 drosophila	Q9V9B9	ъ	183		15
Q9cqu7 mus musculu	09CQU7	11	177		15
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Q9fw22 oryza sativ	Q9FW22	10	173		15
schi	Q27774	u	213		16
Q96ca2 homo sapien	Q96CA2	4	212		16
Q9tw32 dictyosteli	Q9TW32	U3	197	7.7	16

ALIGNMENTS

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Submitted (AN-2002) to the EMBL/GenBank/DDBJ datal Submitted (AN-2002) to the EMBL/GenBank/DDBJ datal PUNCTION; PPIASES ACCELERATE THE FOLDING OF PROSERVED AND AND ACCEPTANCE OF PROPERTY.

-!- CATALVITC ACTIVITY; CIS-TRANS ISOMERIZATION OF PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY; BELONGS TO THE CYCLOPHILIN-TYPE PROPERTY; BC001125; AAH01125.1; --
EMBL; BC008408; AAH0848.1; --
EMBL; BC00800; AAH20800.1; --
HSSP; P23284; ICYN.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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Kainer D.B., Doris P
"Cyclophilin B.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS
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Mammalia; Eutheria;
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PROSITE; PS50072; CSA_PPIASE_2; 1.
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Pred. No.
                                                                                                                                                                                                                                                                                                                      02408DFA7157218C CRC64;
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ches 0;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Lyone P., Ring B., Ring K.H., Waltz C., Whittaker C., Wilming L.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Lyone P., Ra Ra Ra Kana M., Kana 
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  Q01490;
Q01490;
01-NOV-1998
01-NOV-1998
01-DEC-2001
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
Peptidylprolyl isomerase B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002130; CSA_PPIlase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; AK003257; BAB22036.1; - EMBL; BC013061; AAH13061.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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TISSUE-BREAST TUMOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P23284; 1CYN.
MGD; MGI:97750; Ppib.
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                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                      RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 159
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  (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                               216 AA; 23713 MW;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                     PRELIMINARY;
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Created)
Last sequence update)
Last annotation update)
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Best Local S
Matches 37
MOI. Gen. Genet. 266:537-545(2001).

EMBL; AY005867; AAF98447.1; -.

InterPro; IPR002130; CSA_PPIase.
InterPro; IPR000186; ER_target.

Pfam; PF00160; pro_isomerase; 1.

PRINTS; PR00153; CSA_PPIASE.; UNKNOWN_1.

PROSITE; PS00170; CSA_PPIASE_2; 1.

PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
                                                                                                                                                                                                                                                                           08X166 PRELIMINARY;

08X166;

01-MAR-2002 (TrEMBLrel. 20, C

01-MAR-2002 (TrEMBLrel. 21, L

01-JUN-2002 (TrEMBLrel. 21, L

Cyclophilin-like peptidyl pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen H., Li x.-L., Ljungdahl L.G.;

"A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.";

Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).

-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PROTIDE BONDS IN OLIGOPEPTIDES.

-i- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

-i- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Chytridiomycota
Neocallimasticaceae; Orpinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orpinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptidyl-prolyl cis-trans isomerase (Cyclophilin B) (Rotamase).
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PROSITE; PS50072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Signal; Cyclosporin;
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InterPro; IPR002130; CSA_PPIase.
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HSSP; P23284; ICYN.
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                                                                                                                                                                                                             Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                     CYPB.
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                                                                                                                    Aspergillus niger and contains signal HEEL.";
                                                                                                                                              Derkx P.M.F., Madrid S.M.;
"The foldase CYPB is a component of the
                                                                                                                                                                                                 NCBI_TaxID-5061;
                                                                                                                                                                         SEQUENCE FROM N.A.
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37; Conser
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nilarity 100.0%;
Conservative 0
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203
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Pred. No. 1.8
0; Mismatches
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PREVENT SECRETION FROM ER
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A5748C94305B8BE0 CRC64;
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                                                                                                                                   endoplasmic
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Q 2927H Q 2927
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Best Local
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Best Local :
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Q29278;
Q1-NOV-1996
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01-MAY-1999
01-MAY-1999
01-MAR-2002
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SEQUENCE
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NON_TER
SEQUENCE
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01-DEC-2001 (TrEMBLrel. 1:
Cyclophilin B (Fragment).
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mamm. Genome 7:509-517(1996).
EMBL; F14628; CAA23162.1; -.
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-SMALL INTESTINE;
MEDLINE-96327607; PubMed-8672129;
Winteroe A.K., Fredholm M., Davie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                            CYPB
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PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
                      cyclophilin B.";
Fungal Genet. Bi
-i- FUNCTION: PP
                                                                                              SEQUENCE FROM N.A.
MEDLINE-99343878; PubMed-10413615;
Joseph J.D., Heitman J., Means A.R.;
                                                                                                                                                                          Eukaryota; Fungi; Ascomycot
Eurotiales; Trichocomaceae;
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                          Cyclophilin
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                                                                       Joseph J.D., Heitman J., Means A.R.;
"Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluation and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 WLDGKHVVFGKVLEGMEVVRKVESTKTD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ibrary."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WLDGKHVVFGKVLEGMEVVRKVESTKTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50072; CSA_PPIASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AA;
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                        Biol, 27
PPIASES
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100.0%; Pr
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                                               27:55-66(1999)
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Pred. No.
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Last sequence update)
Last annotation updat
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Pred. No.
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3e-21;
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                                                                                  Aspergillus nidulans
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                      -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PEPTIDE BONDS IN OLIGOPEPTIDES.
-1- SIMLIARITY: BELONGS TO THE CYCLOPHILIN-TYPE PP: EMBL; AF078071; AAC64933.1; -1 SIMLIARITY: BELONGS TO THE CYCLOPHILIN-TYPE PP: HSSP; P05092; 2CPL.
InterPro; IPR002130; CSA_PPIASE.
InterPro; IPR002130; CSA_PPIASE.
PF00160; Pro_isomerase: 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
ISOMERASE: ROTAMASE.
ISOMERASE: ROTAMASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR002130; CSA_PPIase.
InterPro: IPR000886; ER_target.
Pfam; PP00160; pro_isomerase; 1.
PRINTS: PR00153; CSAPPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
    Q8X0S3;
Q8X0S3;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ZT54;
Q9ZT54;
Q9ZT54;
Q9ZT54;
Q9ZT54;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Lee Y.K., Hong C.B., Shu Y., Lee I.K.;

Lee Y.K., Hong C.B., Shu Y., Lee I.K.;

"Isolation of a cDNA Clone for Cyclophilins from Griffithsia japonica and Structural Comparison of Cyclophilins.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY STMILARITY).

-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; I
Griffithsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Griffithsia japonica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-83288;
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1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEIASE FAMILY.
EMBL, AF107254; AAD17998.1; -.
HSSP; P23284; 1CYN.
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                                                                                                                                                                              QGGDFTRGDGTGGKSIYGE
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28; Conserv
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162 AA;
(TrEMBLrel.
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                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                    9.1%;
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Created)
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Last sequence update)
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                Indels
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RESULT
OF TOTAL TO
   RX MEDLINE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lai R., Lai
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDB.
EMBL; AL670011; CAD21421.1; -
Interpro; IPR002130; CSA_PPIASE.
Pfan; PF00160; pro_isomerase; 1.
PFINTS; PR00153; CSAPPISMRAE;
PRINTS; PR00170; CSA_PPIASE_1; UNKNOWN_1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 207 AA; 22557 MW; AA0B42D3A8D9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q917V3;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydtoidea; Drosophilidae; Drosophila.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Lei Y.,
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ilidae; Drosophila.
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H.W., Mannhaupt G.;
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he EMBL/GenBank/DDBJ
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0; Mismatches
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5.1e-11
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Prinrs; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2;
SEQUENCE 120 AA; 12962 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P23284; 1CYN.
FlyBase; FBgn0034753; CG2852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
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Q25093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
"CDNA libraries from identified neurons.";
Proc. R. Soc. Lond., B, Biol. Sci. 263:57-62(1996).
-i- FUNCTION: PDIASES ACCELERATE THE FOLDING OF PROTEINS (BY
SIMILARITY).
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
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                                                                                                                                                                                                                                            Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96165729; PubMed=8587897;
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                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U36797;
HSSP; P05092;
                                                                                                                                                                                                               somerase;
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9
                                                                                      Local
95 QGGDFTRGDGTGGKSIYG 112
                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE BONDS IN OLIGOPEPTIDES SIMILARITY: BELONGS TO THE CYCLE; U36797; AAB01531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMANAGKDTNGSQFFITT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conserv
                                                                                         Similarity
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IPR002130; CSA_PPIase.
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                                                               Conservative
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                                                                                                                                                                                      AA.
                                                                                                                                                                                      15398 MW;
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                                                               0;
                                                                                            Score 18;
Pred. No.
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                                                                                                                                                                                         64FFD82018480A6B CRC64;
                                                                   Mismatches
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                                                                                                                         Length 143;
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AC 09W22
AC 00C C2888
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      HSSP; P23284; ICYN.
FlyBase; FBgn0034753; CG2852.
InterPro; IPR002130; CSA_PPIAse.
Pfam; PF00160; pro_isomerase; 1.
PR.NTS; PR00153; CSAPPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                                                            -!- FUNCTION: PPIASES ACCELERATE THE
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                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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093826;
01-MAY-1999 (TEMBLICAL 10,
01-MAY-1999 (TEMBLICAL 10,
01-JUN-2002 (TIEMBLICAL 21,
Eukaryota; Fungi; Ascomycota;
Onygenales; Arthrodermataceae;
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Limulidae;
                                                  Arthroderma benhamiae.
                                                                              Cyclophilin.
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIANE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA)
-!- TISSUE SPECIFICITY: HEMOCYTE LARGE SECRETORY GRANUL
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE
EMBL; AB002814; BAA23764.1; -.
HSSP; P23284; ICYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98019238; PubMed-9353327;
Takaki Y., Muta T., Iwanaga S.;
"A peptidyl-prolyl cis/trans-isomerase (cyclophilin G) in regulated secretory granules.";
J. Biol. Chem. 272:28615-28621(1997).
-I- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. MAY PLAY / ROLE IN MAINTAINING THE CONFORMATIONAL INTEGRITY OF STORED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Peptidyl-prolyl cis-trans isomerase G precursor (EC 5.2.1.8) (PPIase (Rotamase) (Cyclophilin G) (P27).
Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclosporin; Isomerase; Rotamase; Signal; Multigene family SIGNAL 1 23
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01-JUN-1998 (TrEMBLrel.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SMANAGKDTNGSQFFITT
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CATALYTC ACTIVITY: CIS-TRANS ISOMERIZATION
PEPTIDE BONDS IN OLIGOPEPTIDES.
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l Similarity 100.0%;
18; Conservative
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205 AA;
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                    Ascomycota; Pezizomycotina; Eurotiomycetes;
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24198 MW;
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Pred. No.
                                                                                                                                                                                             PRT;
  Arthroderma
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3. 5.7e-10;
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5.4e-10;
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Best Local :
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InterPro: IPRO02130; CSA_PPIase.
Pfam: PF00160; pro_lsomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
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015729;
01-JAN-1998
01-JAN-1998
01-JAN-2002
                                                                    InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPIASE.1; 1.
PROSITE; PS00170; CSA_PPIASE.1; 1.
PROSITE; PS00172; CSA_PPIASE.2; 1.
                                                                                                                               -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
EMBL; AF017993; AAB86601.1; -.
HSSP; P05092; 2CPL.
                                                                                                                                                                                                  "Cloning, characterization and functional expression of Entamoeba histolytica.";
Mol. Biochem. Parasitol. 107:219-225(2000).
-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTE
                                                 Isomerase;
SEQUENCE
                                                                                                                                                                                                                                                                        STRAIN-HM1:IMSS;
MEDLINE-20243663; PubMed-10779598;
                                                                                                                                                                                                                                                                                                                                    Entamoeba histolytica
Eukaryota; Entamoebida
                                                                                                                                                                                                                                                               Ostoa-Saloma P.,
                                                                                                                                                                                                                                                                                                                                                                        Cyclophilin.
                                                                                                                                                                                                                                                    Laclette J.P.;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PROSITE; PS50072; CSA_PPIASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kano R., Nakamura Y., Watanabe S., Tsujimoto H., Hasegawa A.; "Characterization of the cyclophilin of Trichophyton mentagrophytes."; Microbiol. Immunol. 44:51-56(2000).
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  somerase;
                                                                                                                                                                                           SIMILARITY)
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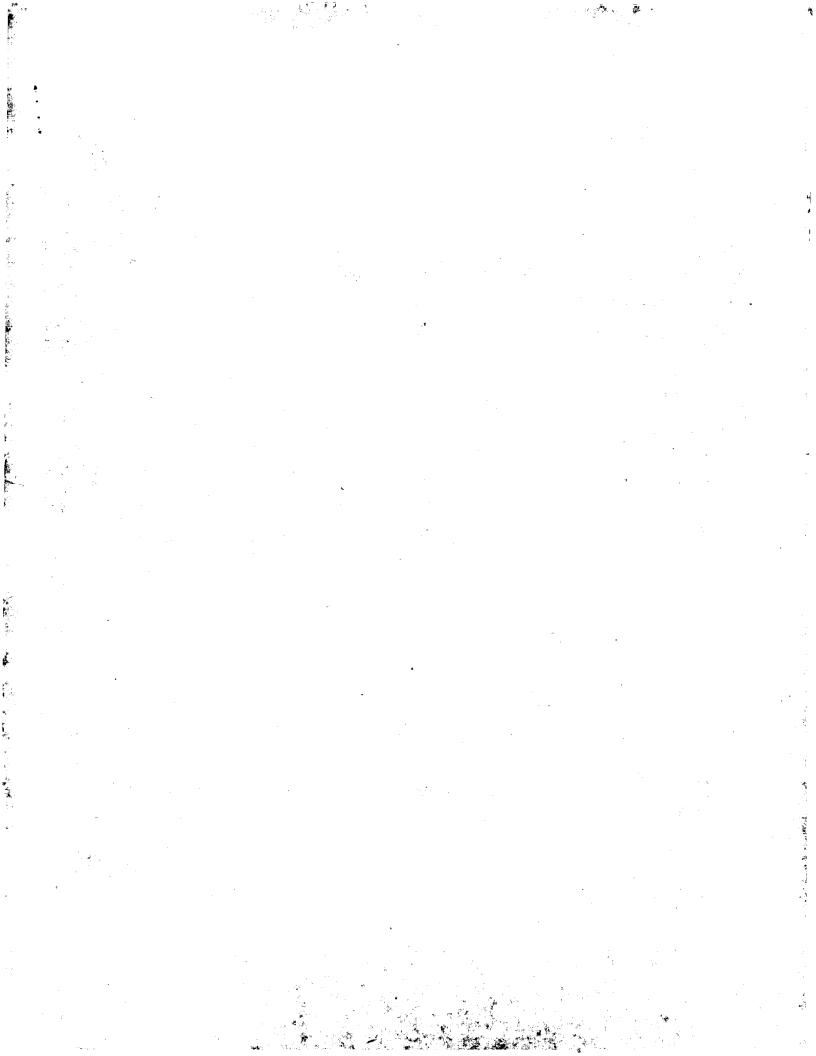
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. printed,

SUMMARIES

10	9	8	7	6	U	4	ω	N	-	Result No.
22	29	64	98	137	183	203	208	208	208	Score
10.6	13.9	30.8	47.1	65.9	88.0	97.6	100.0	100.0	100.0	Query Match
83	212	64	183	166	163	211	291	291	216	Query Match Length DB
22	21	23	22	21	22	22	23	21	22	
AAM24287	AAY92048	AAU99181	AAG65274	AAG00090	AAG65273	AAB73302	ABP41842	AAB43878	ААВ73301	ID
Human EST encoded	A. niger peptidyl-	Partial human pert	Haematopoietic ste	Human secreted pro	Haematopoietic ste	Human cyclophilin	Human ovarian anti	Human cancer assoc	Human cyclophilin	Description

4 .5	4.4	Δ. W	42	41	40	39	38	37	36	ω	34	33	32	31	30		28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	13	13	13	13	13	15	15	15	15	15	15	15	16	16	16	16	18	18
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184	176	169	165	165	165	164	164	163	163	162	152	145	145	145	114	106	754	737	236	228	125	250	214	193	183	183	58	58	212	185	185	180	205	120
23	21	23	22	21	19	22	10	22	12	21	21	16	16	12	22	22	23	22	21	21	21	22	22	23	22	21	22	22	14	22	22	19	22	22
ABP41129	AAG44156	ABP42929	AAU01195	AAG03831	AAW56028	AAG65275	AAP90431	AAG65276	AAR13726	AAG44157	AAG08983	AAR72961		AAR10763	AAB64736	ABG27275	AAE24596	ABG10283	AAG18025	AAG18026	AAG18027	ABG23480	ABG23479	ABP4 2003	ABB66236	AAB56701	31	ABG12991	AAR32353	AAG65278	K)	W807	B592	ABB67378
Human ovarian anti	dopsis thali	Human ovarian anti		Human secreted pro	pr	tic	Cyclophilin. Homo	Haematopoietic ste	0		psis	pepi	peptidyl			Novel human diagno	Human SR-cyp prote				opsis		human diagn	Human ovarian anti	ש	5	Novel human diagno	Novel human diagno			ematopoietic st	D. discoideum cycl		Drosophila melanog

ALIGNMENTS

RESULT 1

AAB73301 standard; protein; 216 AA

AAB73301;

22-MAY-2001 (first entry)

Human cyclophilin B (CypB).

Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia.

Homo sapiens.

WO200113113-A1

22-FEB-2001.

10-AUG-2000; 2000WO-US21789

19-AUG-1999; 99US-0149752

(UYPE-) UNIV PENNSYLVANIA.

Clevenger CV, Rycyzyn MA;

WPI; 2001-211249/21.

Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin

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RESULT 2
AAB43878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The invention relates to a composition for modulating somatolactogenic CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B CC (particularly a CypB mutant in which residues 2-12 of the mature protein CC are absent) or an inhibitor of the interaction of cyclophilin B with a CC somatolactogenic hormone (e.g., prolacti, growth hormone). The invention CC also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for CC diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is CC useful for augmenting somatolactogenic function in the animal, and CC cyclophilin B mutant or a composition comprising an inhibitor of the CC interaction of cyclophilin B with a somatolactogenic hormone, is useful CC for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, CC composition comprising cyclophilin B suseful in the treatment of immunosuppression, CC composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising cyclophilin B mutant or a composition comprising CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic CC cancer; gigantism/acromegaly, and hyperprolactinaemia. The present xx sequence represents human cyclophilin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 208;
                   WO200055350-A1.
                                                                                               dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                          antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
                                                                                                                                                                                                                                                                                                                             Human cancer associated protein sequence SEQ ID NO:1323.
                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB43878 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                          sapiens.
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Pred. No. 4.9e-194;
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antilinflammatory; antithyroid; antiallergic; antibacterial; antiviral; antilinflammatory; antithyroid; antiallergic; antibacterial; coagulant; coagulant; thrombolytic; coagulant; coagula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiastimatic; antirheumatic; antiarthritic;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 1974-1975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acids comprising sequences encoding useful for treating or diagnosing e.g. cancer - \,
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                                                                  the present invention.
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       291 AA;
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RESULT 3
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ID ABP4
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AC ABP4
AC ABP4
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Best Local S
Matches 208
            Human ovarian
                                     22-AUG-2002 (first entry)
                                                               ABP41842;
                                                                                        ABP41842 standard;
                                                                                                                                                       264
                                                                                                                                                                               181
                                                                                                                                                                                                         204
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                                                                                                                                                                                                                                                                                                         1 MKVLLAAALIAGSVFFLLLPGPSAADEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKT 60
                                                                                                                                                                   SRDKPLKDVIIADCGKIEVEKPFAIAKE 208
                                                                                                                                                                                                                                                          VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF
                                                                                                                                                                                                                                                                     VPKTVDNFVALATGEKGEGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF 120
                                                                                                                                                       SRDKPLKDVIIADCGKIEVEKPFAIAKE
                                                                                                                                                                                                                                 KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
                                                                                                                                                                                                       KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                              Conservative
            antigen HTFML39,
                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 208; DB 21; 100.0%; Pred. No. 6.4e-194; tive 0; Mismatches 0;
                                                                                         291
            SEQ
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             ID NO:2974
                                                                                                                                                                                                                                                                                                                                                                                      Length 291;
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                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                          203
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The invention relates to 2175 novel human ovarian antigens (ABP41024) and to cDNAs encoding them (ABQ54131-ABQ56305), and also cencompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to compasses polypeptides 90% identical and polynucleotides 95% identical comprising human ovarian antigen antigen polynucleotides against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, composing, prognosing or preventing various ovary and/or breast-related compasses (e.g., infertility, disorders of pregnancy anovulation, complete ovarian captain concer and breast cancer, and disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic concerts, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic concerts, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic concerts, infections (e.g., congenital and acquired commune disorders (e.g., congenital and acquired commune disorders (e.g., congenital and acquired communed ficiencies, autoimmune ophoritis, systemic lupus crythematosus), conducted ficiencies, autoimmune ophoritis, systemic lupus crythematosus), conducted disorders, neurological disorders, gastrointestinal disorders (e.g., anaemia), cardiovascular disorders, compounds which complete therapy, chromosome mapping, in the conducter ovarian antigen expression or activity. The polynucleotides may disorders, congenital and acquired conducted fices may be used as food additives or to prepare antibodies conducted in disease diagnosis, drug targeting and phenotyping. The present consection of this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO casting antigen of the invention.
         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID No 2974; 2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-147878/19.
N-PSDB; ABQ54919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-2000; 2000US-209467P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory;
       Similarity
                                                                           291
                                                                           A
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    100.0%;
Score 208; DB 23;
Pred. No. 6.4e-194;
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1 MKVLLAAALIAGSVEFLLLPGPSAADEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKT

Matches

Conservative

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Mismatches

Indels

0,

Gaps KT 60

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The invention relates to a composition for modulating somatolactogenic CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B CC (particularly a CypB mutant in which residues 2-12 of the mature protein CC are absent) or an inhibitor of the interaction of cyclophilin B with a CC somatolactogenic hormone (e.g., prolaterin, growth hormone). The invention CC also relates to a method of identifying inhibitors of somatolactogenic control of cyclophilin B with a somatolactogenic hormone, and a method for CC diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB and a sample from a patient. Cyclophilin B is cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin B with somatolactogenic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature muscle wasting; osteoporosis; HIV infection; breast cancer; prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page -; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-211249/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clevenger CV, Rycyzyn MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        somatolactogenic hormone
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Best Local
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                                        Query Match
Best Local Similarity
Matches 183; Conserv
                                                                                                    The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaemopoiesis in radiotherapy and chemotherapy of various haematopoietic organ diseases and cancers. The present sequence is a human protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                          JP2001163798-A
                                                                                                                                                                                                                                                                                                                                                                 Haematopoietic stem cell proliferation dyshaemopoiesis; cancer; human; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG65273
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG65273 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The present sequence is not shown in the specification, but is derived from the wild-type CypB sequence shown on pages 17-18.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 Haematopoietic
                                                                                 Sequence
                                                                                                                                                                    Claim
                                                                                                                                                                                                  Proliferation
                                                                                                                                                                                                                                                              03-DEC-1999;
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                                                                                                                                                                                                                                         (KANF ) KANEKA CORP
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DEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKF
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                                      88.0%;
nilarity 100.0%;
Conservative 0
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Pred. No.
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                                          Mismatches
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                                                   DB 22; 1
8.8e-170;
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Matches 137;
                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                     The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30' different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr prined cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 4171; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
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DB; AAC00096.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITTVKTAWLDGKHVVPGKVLEGMEVVRKVESTKTDSRDKPLKDVIIADCGKIEVEKPFAI 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5' EST;
                                                                                                                                  Similarity
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                                                                                                                                Score 137;
Pred. No.
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                                                                                                                                  DB 21;
4.5e-125;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaempoiesis in radiotherapy and chemotherapy of various haematopoietic organ diseases and cancers. The present sequence is a murine protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG65274 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proliferation agent for hematopoietic stem cell containing cyclophilin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haematopoietic stem cell proliferation
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                       Partial human perturbagen F802
                                                                              24-SEP-2002 (first entry)
                                                                                                                                       AAU99181
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                                                                                                                                                                                            AAU99181 standard; Protein; 64 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFDDENF
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGE 88
                                                                                                                                                                                                                                                                                                                                    RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 14; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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DB 23; 1.9e-54; 0;

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Sequence

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CC polypeptide, screening (M) putative RA related therapeutics, by exposing the RA pathway polypeptide, to a number of agents, and recovering a cc subpopulation of disrupting agents which competitively displace the cc subpopulation of disrupting agents which competitively displace the cc polypeptide from the target, where the disrupting agents are putative RA related therapeutics. Also include are an isolated RA pathway polypeptide comprising PAT1 (a kinesin light chain related protein) polypeptide cand its encoding polynucleotide, a gene therapy vector comprising the RA cc pathway protein polypeptide or encoding or PAT1 and a host cell comprising the gene therapy vector. The RA pathway polypeptide is useful comprising the gene therapy vector. The RA pathway related collecting reporter expression, where that interacts with RA pathway-related collecting reporter expression, where the reporter expression is coperatively linked to the formation of the interaction pair, by coperatively linked to the formation of the interaction pair (M) is a coperatively linked to the formation of the interaction pair treating comparatively particle cancer, percent vector, pair cancer, covarian cancer, dermatitis, hyperkeratosis, eczema, Darier's disease, covarian cancer, dermatitis, hyperkeratosis, eczema, Darier's disease, psoriasis, acute promyelocytic leukaemia (APL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retinoic acid pathway; RA; retinoid; lung cancer; neuroblastom Karposi's sarcoma; breast cancer; pancreatic cancer; neuroblastom renal cancer; ovarian cancer; dermatitis; hyperkeratosis; eczema; barier's disease; Reiter's disease; psoriasis; gene therapy; F797 acute promyelocytic leukaemia; APL; Perturbagen; R3; F802; F820; acute promyelocytic leukaemia; APL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Also included are the polynucleotides encoding the perturbagens, a vector comprising the polynucleotide, preparing an RA pathway related polypeptide, a composition comprising the polypeptide, a composition comprising the polypeptide, screening (M) putative RA related therapeutics, by exposition polypeptide, screening (M) putative RA related therapeutics, by expositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polypeptide (I) with retinoic acid (RA) pathway activity, comprising a polypeptide sequence of Perturbagen (phenotypic probe) R3, Perturbagen F802, Perturbagen F802, their biologically active modifications, or biologically active fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide with retinoic acid pathway activity, especially of perturbagens R3, F802 and F820 for identifying a cellular targetinteracts with the polypeptide and for therapeutic purposes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 13a; 131pp; English.
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                                                                                                                                        Query Match
Best Local s
Matches 29
                                                                                                                                                                                                       This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans isomerization of a peptide bond on the N-terminal side of proline residues in polypeptides. CYPB are useful in methods for increasing the yield of secreted polypeptides from cells. The secreted polypeptides may be enzymes (such as chymosin, thaumatin or alpha-galactosidase) that can be used in food processing, a pest toxin, adenosine diphosphate (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
            AAM24287;
                                 AAM24287 standard;
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                     Claim 13; Page 47-48; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                     New peptidyl prolyl cis-trans isomerase, designated CYPB, from Aspergillus niger, useful in methods for increasing the yield of secreted polypeptides, such as enzymes used in food processing, from
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-293167/25.
N-PSDB; AAA08772.
                                                                                                                                                                                                                                                                                                                                               cells
                                                                                                                                                                                                                                                                                                                                                                                                                                            Derkx PMF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase;
beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclophilin-like peptidyl prolyl cis-trans isomerase; Cyrfood processing; Endoplasmic retention signal; cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200018934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. niger peptidyl-prolyl cis-trans isomerase (CYPB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY92048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY92048 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                             84
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                                                                                         FHRVIKDFMIQGGDFTRGDGTGGKSIYGE 113
                                                                                                                                                      Similarity
                                                                                                                                                                                       212 AA;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Madrid SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-IB01669
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24.212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                     13.9%;
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                                  83
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                                                                                                                                                      Score 29;
Pred. No.
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                                                                                                                                         Mismatches
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ches 0;
                                                                                                                                                             Length 212;
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RESULT 11

ABB67378

ID ABB67
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Best Local
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03-AUG-2000;
15-SEP-2000;
                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, plg, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                     W0200171042-A2
                                          Drosophila melanogaster.
                                                                                                  Drosophila
                                                                                                                                                 ABB67378;
                                                                                                                                                                       ABB67378 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 1183-1184; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476164/51.
N-PSDB; AAH98946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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22; Conser
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Drmanac RA,
                                                                                                melanogaster polypeptide
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; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                        AA;
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A, Zhang
                                                                                                                                                                       Protein;
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J, W
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Werhman
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                                                                                                  SEQ ID NO 28926
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an T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, raising
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RESULT 12
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                         N-PSDB; ABL03400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila
                                                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic a genes from Drosophila interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 SMANAGKDTNGSQFFITT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072)
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                            2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMANAGKDINGSOFFITT 56
                                                                                     JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
18; Conserv
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                                                                                     Adams M,
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Pred. No.
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J. 1.9e-09;
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and cell-cell
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RESULT 13
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This represents the amino acid sequence of cyclophilin (DdCyP2) from the DictyOstelium discoldeum Ax-2. The invention provides sequences encoding DictyOstelium DDI, human DPI (hDP1) and DictyOstelium cyclophilin (DdCyP2) which are bisphosphonate binding proteins. The invention also provides methods for purifying and producing such bisphosphonate binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cook JS,
Russell
                                                                                                                                                                                                                                                                                              Bisphosphonate binding protein - used disorders, including bone metabolism, metastases, and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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(UYSH-) UNIV SHEFFIELD MED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1998;
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DB; AAV56008.
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaemopoiesis in radiotherapy and chemotherapy of various haematopoietic organ diseases and cancers. The present sequence is a human protein described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proliferation agent for hematopoietic stem cell containing cyclophilin
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Best Local :
                                       Matches
                                                                                               The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatmen of dyshaemopoiesis in radiotherapy and chemotherapy of various haematopoietic organ diseases and cancers. The present sequence is a murine protein described in the exemplification of the invention.
                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                Haematopoietic stem cell dyshaemopoiesis; cancer;
                                                                                                                                                                                            proliferation agent for hematopoletic stem cell containing cyclophilin
                                                                                                                                                                                                                                                           03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                      JP2001163798-A.
                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                               dyshaemopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                             Haematopoietic stem
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                                                                                                                                                               Disclosure;
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                                                                               Sequence
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                                               Local
60 FHRVIKDFMIQGGDFT
          FHRVIKDFMIQGGDFT
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                                       16; Conservative
                                                                                185 AA;
                                                                                                                                                               Page 17; 19pp;
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                                                                                                                                                                                                                                                                               99JP-0345542
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                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation agent related murine
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                                                                                                                                                                                                                                                                                                                                                                proliferation agent;
human; mouse.
                                                                                                                                                                Japanese.
                                         0;
                                        Score 16; DB
Pred. No. 2.4
0; Mismatches
                                                   DB 22;
2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                           cyclophilin;
                                          0;
                                                           Length 185
                                          Indels
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                                          0;
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Result
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB seq
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length: 2000000000
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                             /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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       GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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US-08-145-995A-9
US-08-145-995A-9
US-08-145-995A-8
US-08-145-995A-8
US-08-145-995A-16
US-08-145-995A-16
US-08-145-995A-6
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US-08-145-995A-16
US-08-145-995A-16
US-08-145-995A-14
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Query Match
Best Local Similarity
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Score 208; DB 1; Pred. No. 1.4e-188;

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US-08-482-728A-10
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                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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110 IYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGME 169
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STATE: California
                                                                                                               Watch 60.6%; So Local Similarity 100.0%; I hes 126; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                 STREET:
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                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                 TOPOLOGY:
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Pred. No. 1.9e-111;
0; Mismatches 0;
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US-08-142-897-5
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                                                                                                                                            Sequence 5, Application US/08142897
Patent No. 5447852
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Best Local
                                                                                                                                                                                                                                                                                                             Matches
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TELEFAX: (415) 398-324
TELEX, 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Silva, Robin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: un
MOLECULE TYPE:
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APPLICANT: Payan, Donald
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                 APPLICANT: Friedman, Jeffrey S. APPLICANT: Weissman, Irving L. TITLE OF INVENTION: NO. 547852
TITLE OF INVENTION: and Uses
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                                                  NUMBER OF SEQUENCES:
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CITY: San Francisco
STATE: California
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REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                           83 SKFHRVIKDFMIQGGD 98
                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 amino acids
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                                                                    Irving L.
No. 5447852el Cyclophilins, Associating Proteins
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COUNTRY:

USA

San Francisco California

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US-08-142-897-6
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                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                             APPLICATION NUMBER: (FILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza,
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NO. 5447
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 01 FILING DATE: 15-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             APPLICATION NUMBER: US 0 FILING DATE: 15-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                   San Francisco
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Weissman, Irving L.
VENTION: No. 5447852el Cyclophilins, Associating Proteins
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                                US 08/005,917
                                                                                                      US/08/142,897
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Pred. No.
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                                                                                                                                                                                                                                                                                                 Steuart Tower, Suite 2000
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US-08-482-728A-9
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US-08-482-728A-9
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                                                                                                                     TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                         APPLICATION NUMBER: US/08/482
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SILVA, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                         TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                      TYPE:
                                 TOPOLOGY:
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: si
TOPOLOGY: linear
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REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 54
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                                   unknown
                protein
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Best Local Similarity

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Score 12; Pred. No.

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                                                                                                                     RESULT 8
US-08-145-995A-9
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GENERAL INFORMATION:
APPLICANT: CARLOW, CAPPLICANT: PAGE, ANTITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                    Sequence 9, Application US/08145995A Patent No. 5482850
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Best Local (
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAA-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Friedman, Jeilrey
APPLICANT: Weissman, Irving
TITLE OF INVENTION: NO. 5447B
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
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                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                        104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
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                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                          Similarity
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amino acid
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               415-326-2422
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                                    PAGE, ANTONY
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linear
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                                                    CARLOW, CLOTILDE K.S.
                                                                                                                                                                                                                                                                                                                                           protein
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METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/142,897
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                                                                                                                                                                                                                                                                         Score 12; DB 1; L; Pred. No. 0.00074;
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                                                                                                                                                                                                                                                                                          Length 163;
                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08451747 Patent No. 5821107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: CARLOW, CLOTILDE K
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 WLDGKHVVFGKV 132
                                                 APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/OFFILING DATE: 29-OCT-1993
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                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 164 amino acids
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12; Conservative
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                                                                                                                                                                                                                                                            BEVERLY
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                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                            GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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                                                                                                                                                                                                                                                                                                                                                                                              CLOTILDE K.S
                                                                                                                                                                                                                                                                                                                                                               METHOD FOR IDENTIFYING ANTI-PARASITIC
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                                                                                      US/08/451,747
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; Pred. No.
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Length 164; Indels

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Best Local Similarity 100.0%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 164 amino acid
                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/145,995
FILING DATE: 29-OCT-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acid
                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 21
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARLOW, CLOT
APPLICANT: PAGE, ANTONY
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                                                                                                                                                                                        NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unl
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              TOPOLOGY:
                               TYPE: amino acid
STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                             164 amino acids
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Pred. No.
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US-08-145-995A-8
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                                                                                                                  RESULT 12
US-08-451-747-8
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                                                                                     Sequence 8, Application US/08451747 Patent No. 5821107
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5482850
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APPLICANT: CARLOW
APPLICANT: PAGE,
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 523-644
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, V CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/145,995A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            APPLICANT: CARLOW, CLOT:
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METI
TITLE OF INVENTION: COM
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ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                  Match 5.8%;
Local Similarity 100.0%;
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                                                                                                                                                                             WLDGKHVVFGKV 132
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                                                          CARLOW, CLOTILDE K.S.
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METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS 21
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Pred. No
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Pred. No.
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CORRESPONDENCE ADDRESS:

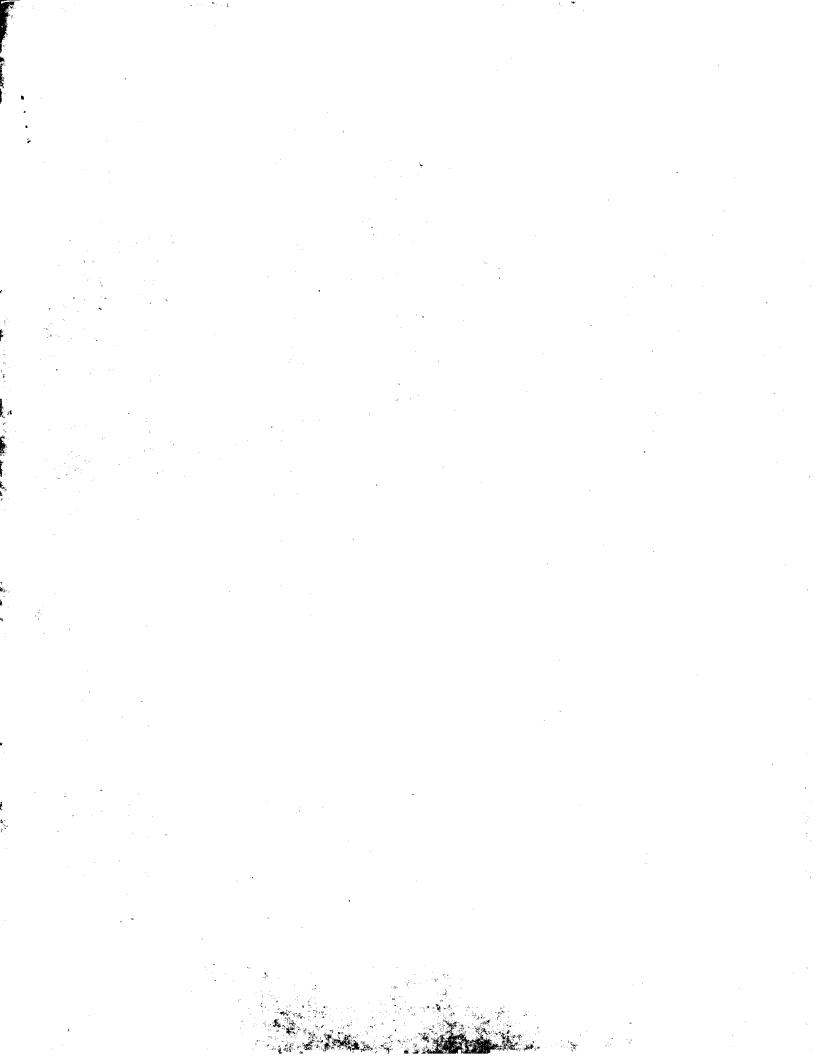
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RESULT 13
US-09-134-852-8
; Sequence 8, Application US/09134852
; Patent No. 6127148
; Patent No. 6127148
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TOPOLOGY: unknown;
MOLECULE TYPE: protein
US-08-451-747-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/1/
FILING DATE: 29-OCT-1993
FLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR I
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5554
TELEPHONE: (508) 927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
CLASSIFICATION:
                                                                                                                                                                          COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                   CITY: BOSTON
                                                                                                                                                                                                                                                                     ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
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5.8%; Score 12; DB 2; I
Local Similarity 100.0%; Pred. No. 0.00075;
les 12; Conservative 0; Mismatches 0;
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CITY: BEVERLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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RESULT 14
US-08-482-728A-16
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TOPOLOGY: unknown;
MOLECULE TYPE: protein
US-09-134-852-8
                                                     TELECHONE: (415) /ox --
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08482728A Patent No. 5968802
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APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 1
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOPOLOGY: u
MOLECULE TYPE:
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APPLICATION NUMBER: US 08
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 WLDGKHVVFGKV 132
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/482,728A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
ADDRESSEE: Four Embarcadero Center, Suite 3400
                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
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Local Similarity 100.0%;
nes 12; Conservative (
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94111-4187
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RESNICK, DAVID S.
WIMMER: 34235
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 781-1989
TELEFAN: (415) 781-1989
TELEFAN: (415) 781-1989
TELEFAN: (415) 781-1989
INFORMATION FOR SEQ ID NO: 13:
SBOUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                   ; STRANDEDNESS: unknown
TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-13
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Search completed: April 10, 2003, 11:56:00 Job time : 16 secs
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US-08-482-728A-13
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Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.3%; Score 11; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 0.0052; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         Query Match 5.3%; Score 11; DB 2; Length 134 Best Local Similarity 100.0%; Pred. No. 0.0055; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                   98 TNGSOFFITTV 108
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CITY: San Francisco
STATE: California
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ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
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Maximum DB seq length: 2000000000
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Query
Match
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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           В
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0 US-09-864-761-40591

US-10-128-072-8

US-10-121-049-8

US-10-121-049-8

US-10-175-746-8

US-10-176-918-8

US-10-176-918-8

US-10-176-918-8

US-10-177-965-8

US-10-177-965-8

US-10-140-474-8

US-10-140-474-8

US-10-143-114-8

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US-10-143-114-8

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US-10-143-114-8
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Sequence 12, Appl
Sequence 13, 3, App
Sequence 11, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 8, Appli
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ery M st Lo tches 1 61 61 121 121	10 043		220 220 221 222 222 222 222 222 222 222
N X-X <-< Z-Z D+	ESULT 1 S-10-043-142-12 S-quence 12, Application US/1 Patent No. US20020150959A1 PATENT NO. US20020150959A1 PAPLICANT: DERKX, PATRICK M. APPLICANT: MADRID, SUSAN M. TITLE OF INVENTION: PEPTIDYL FILE REFERENCE: 078883/0128 CURRENT FILING DATE: 2002-0 PRIOR FILING DATE: 2002-0 PRIOR FILING DATE: 1999-09-3 PRIOR APPLICATION NUMBER: PC PRIOR APPLICATION NUMBER: GB PRIOR APPLICATION NUMBER: GB PRIOR APPLICATION NUMBER: GB PRIOR FILING DATE: 1998-09-3 PRIOR APPLICATION NUMBER: GB PRIOR FILING DATE: 1998-09-3 NUMBER OF SEQ ID NOS: 12 SOFTMARE: PATENTLY OF TAMES LENGTH: 208 TYPE: PAT ORGANISM: Homo Sapiens S-10-043-142-12		100 1100 1100 1100 1100 1100 1100 1100
ch 1 Similarity 208; Conservat KVLLAAALIAGSVFF 	plicat 020150 XION: XION: DXID: DATE: DATE: 1 DATE: 2 DATE: 2 DATE: 2 DATE: 1 ION NU ATE: 1 ION NU ATE: 1		444444000000000000000000000000000000000
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Score 208; DB 12; Leng Pred. No. 9.2e-190; Df Mismatches 0; Inde AADEKKKGPKVTVKVYFDLRIGDEDV AADEKKKGPKVTVKVYFDLRIGDEDV AADEKKKGPKVTVKVYFDLRIGDEDV AADEKKKGPKVTVGGGDFTRGDGTGGKE [043142 PROLYL CIS-TRANS ISOMERASES S/10/043,142 -14 -1806,399 /IB99/01669 9821198.0	ALIGNMENTS	US-10-142-419-8 US-10-123-262-8 US-10-141-755-8 US-10-141-755-8 US-10-141-755-8 US-10-141-755-8 US-10-143-032-8 US-10-143-032-8 US-09-738-626-3329 US-09-738-626-3329 US-09-949-192-51 US-09-949-192-51 US-09-949-192-51 US-09-9415-242-10261 US-09-9815-242-10261 US-09-9815-242-1085 US-09-738-626-440-3 US-09-738-626-440-3 US-09-738-626-440-3 US-09-468-147-16 US-09-986-480-195
FGKT IIII FGKT DENF DENF DENF DENF			Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 12, Appli Sequence 12, Appli Sequence 1339, Ap Sequence 5320, Ap Sequence 51, Appli Sequence 10261, A Sequence 14085, Ap Sequence 292, Appli Sequence 292, Appli Sequence 4103, Ap Sequence 4103, Ap Sequence 41050, Appli Sequence 45050, A Sequence 36135, Appli Sequence 3193, Appli
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TATLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30
PRIOR FILING DATE: 1909-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
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; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (57)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
us-09-925-301-1323
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US-10-043-142-11
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Best Local Similarity 100.0%;
Matches 208; Conservative (
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LENGTH: 291
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
SOFTWARE: PatentIn Ver.
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD 263
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Pred. No. 1.2e-189;
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; LENGTH: 207
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-043-142-11
                                                                                                                        CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: GB 9821198.0
PRIOR APPLICATION NUMBER: GB 9821198.0
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
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; ORGANISM: Aspergillus niger
US-10-043-142-5
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LENGTH: 207
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Best Local Similarity
Matches 55; Conserva
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Best Local S
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                                                                                      SEQ ID NO 5
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APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
CURRENT FILING DATE: 2002-01-14
                                                                                                                                                                                                                                                                                                                             APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 9821198.0 PRIOR FILING DATE: 1998-09-30 NUMBER OF SEQ ID NOS: 12
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PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
                                                                                                        SOFTWARE: PatentIn Ver.
                                           TYPE: PRT
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                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 37; Conserv
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100.0%; Pred. No.
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b; Pred. No. 1.7
0; Mismatches
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. 1.7e-27;
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1.4e-44;
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; Sequence 1279, Application US/09925300
; Patent No. US200220151681A1
; GENERAL INFORMATION:
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SEQ ID NO 1279
LENGTH: 183
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Best Local :
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                                                                               PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Craig Rosen, APPLICANT: Steve Ruber
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                       PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: Aeomica-X-1
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                                     APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                              FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
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Hanzel, David K.
Chen, Wensheng
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Pred. No.
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Pred. No.
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. 6.8e-20;
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RESULT 8
US-10-028-072-8
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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APPLICANT: Baker, Ke
APPLICANT: Beresin
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                                 APPLICANT: Wood, Wil
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
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CURRENT APPLICATION NUMBER: US/10/028,072
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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Watanabe, Colin K
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Filvaroff, Ellen
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NN: EXPRESSED IN LUNG, SIGNAL = 3.2

AULT LIVER, SIGNAL = 2.8

NN: EXPRESSED IN HEART, SIGNAL = 3.6

NN: EXPRESSED IN BRAIN, SIGNAL = 1.5

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6

NN: EXPRESSED IN HELA, SIGNAL = 1.6

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PRIOR APPLICATION NUMBER: 50/062250 PRIOR FILING DAVE: 1997-10-17 PRIOR PRIOR PRICAPTION NUMBER: 60/062287 PRIOR PRICAPTION NUMBER: 60/062287 PRIOR APPLICATION NUMBER: 60/062814 PRIOR APPLICATION NUMBER: 60/062816 PRIOR APPLICATION NUMBER: 60/063045 PRIOR PRICAPTION NUMBER: 60/063045 PRIOR APPLICATION NUMBER: 60/063045 PRIOR APPLICATION NUMBER: 60/063082 PRIOR PILING DATE: 1997-10-24 PRIOR APPLICATION NUMBER: 60/063082 PRIOR APPLICATION NUMBER: 60/063082 PRIOR PILING DATE: 1997-10-27 PRIOR PILING DATE: 1997-10-26 PRIOR PILING DATE: 1997-10-27 PRIOR PILING DATE: 1997-10-29 PRIOR PILING DATE: 1997-10-	ENT FILING DATE: 2001-12 R APPLICATION NUMBER: 60/ R FILING DATE: 1997-06-18 R APPLICATION NUMBER: 60/ R FILING DATE: 1997-08-26 R APPLICATION NUMBER: 60/ R APPLICATION NUMBER: 60/ R FILING DATE: 1997-09-17 R APPLICATION NUMBER: 60/ R FILING DATE: 1997-09-18 R APPLICATION NUMBER: 60/ R FILING DATE: 1997-09-19 R APPLICATION NUMBER: 60/
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US-10-121-049-8
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PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1017
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
PILOT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENGTH: 166
TYPE: PRT
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
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Best Local
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FILING DATE: 19/98-06-11
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-10
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
Wood, William
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Stewart, Timothy A.
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-123-904-8
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US-10-140-470-8
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US-10-123-904-8
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Best Local S
Matches 10
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APPLICANT: Baker, Kevin P.
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LENGTH: 166
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GENERAL INFORMATION
                                                                                                                                                                       Sequence 8, Application US/10140470 Publication No. US20030022331A1
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                           57 IKDFMIQGGD 66
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                                                                                                                                                         INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                             Beresini, Maureen
DeForge, Laura
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Wood, William
                                                       Gerritsen, Mary E.
                                                                        Gao, Wei-Qiang
                                                                                    Filvaroff, Ellen
                                                                                                   Desnoyers, Luc
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100.08; Fi
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100.0%; Pred. No.
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Pred. No.
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0.058;
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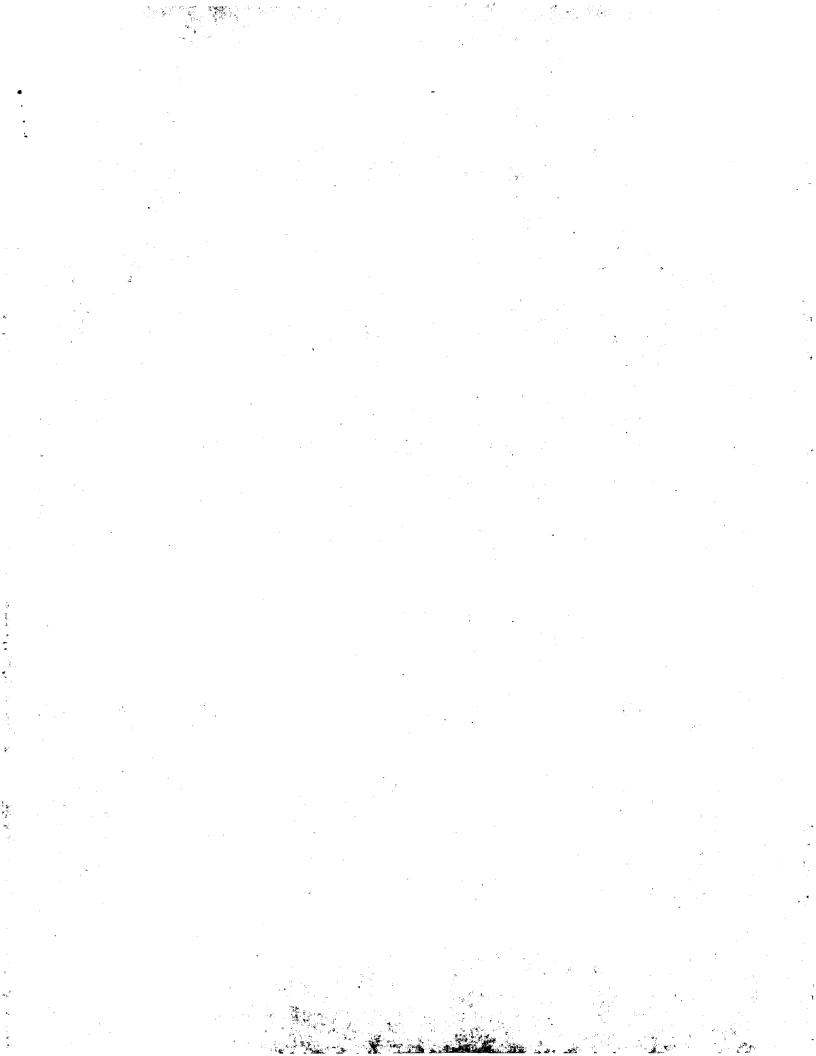
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APPLICANT

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; SEQ ID NO 8
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-8
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; TYPE: PRT
; ORGANISM: HOMO S
US-10-140-470-8
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US-10-175-746-8
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RESULT 13
US-10-176-918-8
                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353
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NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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                                                              57 IKDEMIQGGD 66
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Stewart, Timothy A.
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Filvaroff, Ellen
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                                                                                                                           4.8%; Score 10; DB
100.0%; Pred. No. 0.0
1ve 0; Mismatches
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Pred. No.
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0.058;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENGTH: 166
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-918-8
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US-10-176-921-8
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             Prior Application removed - NUMBER OF SEQ ID NOS: 550 SEQ ID NO 8
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File W
                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
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LENGTH: 166
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No. US20030027275A1
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Wood,William
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Stewart, Timothy A.
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Pred. No.
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0.058;
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APPLICANT: Wood, William
APPLICANT: Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
SEQ ID NO 8
LENGTH: 166
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-865-8
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Search completed: April 10, 2003, 11:56:23 Job time : 18 secs
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; ORGANISM: Homo Sapien
US-10-176-921-8
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US-10-137-865-8
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Publication No. US20030032155A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                  Query Match 4.8%; Score 10; DB 9; Length 166; Best Local Similarity 100.0%; Pred. No. 0.058; Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 10; Conservative (
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                                                                57 IKDFMIQGGD 66
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Victoria
Stewart, Timothy A.
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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peptidylprolyl iso	20k cyclophilin -	peptidylprolyl iso													

ALIGNMENTS

CSHUB

A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell F;1-25/Domain: signal sequence #status predicted <SIG>

C; Function:

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peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat
N;Alternate names: cyclophilin B; ppTaSE
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S71547
R;Ruccknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G.
submitted to the Protein Sequence Database, November 1996
A;Reference number: S71547
A;Molecule type: protein
A;Residues: 1-183 <RUE>
A;Experimental source: liver
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Reywords: cis-trans-isomerase
F;1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <A
peptidylprolyl isomerase (EC 5.2.1.8) Cyp-S1 precursor - mouse
N;Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
C;Accession: A56861; B39722; S21835
R;Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
Biochim. Biophys. Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-S1; a variant peptidyl-prolyl isomerase with a putative:
A;Reference number: A56861; MUID:92096454; PMID:1756174
A;Accession: A56861
A;Accession: A56861; MUID:92096454; PMID:1756174
A;Accession: A56861
A;Residues: 1-216 <SCH>
A;Experimental source: teratocarcinoma F9 cells
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F:35-197/Domain: cyc
F:140/Binding site:
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A; Residues: 1-207 <CAR>
A; Cross-references: GB:M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
A; Cross-references: GB:M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C; Superfamily: peptidylproly1 isomerase; cyclophilin homology
C; Keywords: cis-trans-lsomerase; cyclosporin A binding
E; 34-196/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 266, 107. A;Title: S-cyclophilin. A;Reference number: A40
                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptidylprolyl isomerase (BC 5.2.1.8) (S-cyclophilin) precursor - G:Species: Gallus gallus (Chicken) C:Date: 28-reb-1992 #sequence_revision 28-reb-1992 #text_change 16 C:Accession: A40516
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A; Reference number: S21835
A; Accession: S21835
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A; Note: parts of this sequence, including the amino end of the mature profiles of the sequence, including the amino end of the mature profiles.

R; Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.

Mol. Cell. Biol. 11, 3444-3491, 1991
A; Title: An endoplasmic reticulum-specific cyclophilin.
A; Reference number: A39722; MUID:91260697; PMID:1710767
A; Accession: B39722
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A; Residues: 9-216 < NOR>
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A; Residues: 9-216 <HAS>
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                          A; Accession: A40516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                         114 RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGM
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REPDENEKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGM
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                                                                                                                  Similarity
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100.08;
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%; Pred. No. 8.3
0; Mismatches
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Pred. No.
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7.9e-46;
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peptidylprolyl isomerase (EC 5.2.1.8) B - bovine (1 N;Alternate names: cyclophilin B C;Species: Bos primigenius taurus (cattle) C;Date: 25-Dec:1994 #sequence_revision 14-Jul-1995 C;Accession: S45724

(fragment)

#text_change

11-Jun-1999

RESULT S45724

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peptidylprolyl isomerase (EC,5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegan N;Contains: cyclophilin C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000 C;Accession: T21587 R;Cottage, A. R;Cottage, A. Status: preliminary; translated from GB/EMBL/DDBJ A;Reference number: Z19446 A;Residues: 1-204 KMIL> A;Residues: 1-204 KMIL> A;Cross-references: EMBL: Z92784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1 A;Experimental source: clone F31C3 C;Genetics: A;Gene: CESP:F31C3.1 A;Map position: 1 A;Map position: 1 A;Map position: 1 A;Map cost-tains-1somerase; cyclophilin homology C;Reywords: cis-trans-1somerase F;28-190/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus
N;Alternate names: cyclophilin A; cyclosporin A-binding protein
C;Species: Streptomyces chrysomallus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: S28020; S25676
R;Pahl, A; Uehlein, M; Bang, H.; Schlumbohm, W.; Keller, U.
Mol. Microbiol. 6, 3551-3558, 1992
A;Title: Streptomycetes possess peptidyl-prolyl cis-trans isomerases that strongly resem
A;Reference number: S28020; MUID:93116593; PMID:1474897
A;Accession: S28020
A;Molecule type: DNA
A;Residues: 1-155 <PANI>
A;Cross-references: EMBL:215137; NID:946835; PIDN:CAA78840.1; PID:946836
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;2-165/Domain: cyclophilin homology <CYP>
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A;Molecule type: protein A;Residues: 1-46 <GAL>
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding
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    Query Match
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Pred. No.
  Score 17;
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Pred. No.
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9.5e-11
DB 2;
1e-08;
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                   Length 204;
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A;Cross-references: GB:M74227; NID:g192898; PIDN:AAA37511.1; PID:g192899 C;Comment: This protein binds the immunosuppressive drug cyclosporin A. C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding F;37-199/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                           Cell 66, 799-806, 1991
A;Title: Two cytoplasmic candidates for immunophilin action are A;Reference number: A40047; MUID:91347379; PMID:1652374
A;Accession: A40047
                                                                                                                                                                                                                                                                                                       peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 C;Accession: A40047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase F;25-187/Domain: cyclophilin homology <CYP>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-212 <FRI>
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A; Map position: 3
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T18573
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A; Introns: 66/3
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A;Experimental source: strain Bristol N2
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A; Residues: 1-201 <TAI>
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A; Residues: 1-201 < PAG>
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     l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                    J.; Weissman,
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                     7.7%; Score 16; 100.0%; Pred. No.
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RESULT 11
S46488
                                                                                   RESULT 12
T27371
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C;Superfamily: peptidylprolyl isomerase; cyclophilin hc
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;37-199/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A54204
R;Schmelder, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zuri Blochemistry 33, 8218-8224, 1994
A;Title: Human cyclophilin C: primary structure, tissue distribution, A;Reference number: A54204; MUID:94304830; PMID:8031755
A;Accession: A54204
    pept1dylprolyl isomerase (EC 5.2.1.8) Y75B12B.2 [similarity] -
N;Contains: cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding
                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 300, 871-8/5, 1994
A;Title: The characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase
A;Reference number: S46488; MUID:94280416; PMID:8010972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Bose, S.; Muecke, M.; Freedman, R.B. Blochem. J. 300, 871-875, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: peptidylprolyl cis-trans-isomerase
N;Contains: cyclophilin
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Jul-1995 #sequence_revision 25-Jul-1996 #text_change
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C;Date: 22-Oct-1994 #sequence_revision
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A; Residues: 1-20 <BOS>
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A;Accession: S46488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidylprolyl isomerase (EC 5.2.1.8) - bovine (fragment)
N;Alternate names: peptidylprolyl cis-trans-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:136196; OMIM:123842
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A;Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-212 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
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15; Conservative 0;
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#sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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Pred. No.
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Pred. No.
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9.9e-08;
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                                                                                                                                                                                                                                                                                       Length 20;
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peptidylprolyl isomerase (EC 5.2.1.8)
N;Alternate names: cyclophilin 1; pept
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14

l.8) 1 - Chlamydomonas reinhardtii
peptidyl-prolyl cis-trans isomera

isomerase

71 FHRVIKDFMIQGGDF

85

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peptidylprolyl isomerase (EC 5.2.1.8) c
%;Contains: cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Cct-1999 #sequence_revision
C;Accession: T18578; T24269
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T18578
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A;Introns: 23/3; 107/3
C;Superfamily: peptidylprolyl isomerase; cyclophilin C;Keywords: cis-trans-isomerase
F;3-171/Domain: cyclophilin homology <CYP>
                                                                                                            C;Keywords: c1s-trans-rounce.....
F;16-183/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1995 A; Reference number: Z19867 A; Accession: T24269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A; Reference number: Z20360 A; Accession: T27371
                                                                                                                                                A;Map position: 2
A;Introns: 34/3; B97/3; 148/1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-183 <WIL>
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A;Molecule type: mRNA
A;Residues: 1-183 <PAG>
                                                                                                                                                                                                                            A; Gene: CESP: cyp-11
                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:266499; PIDN:CAA91297.1; GSPDB:GN00020; A;Experimental source: clone T01B7
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85 FHRVIKDFMIQGGDF
                                                                      Local
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15; Conserv
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                                                  red. No. 8.3e-07;
Mismatches 0;
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                                                                                          Length 183;
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A;Gene: TP0947
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
E;34-206/Domain: cyclophilin homology <CYP>
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Search completed: April 10, 2003, 11:55:39 Job time: 21 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-215 <COL>
A;Cross-references: GB:AE001263; GB:AE000520; NID:g3323266; PIDN:AAC65904.1; PID:g332326
A;Experimental source: strain Nichols
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;3-171/Domain: cyclophilin homology <CYP>
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C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T07950
R;Somanchi, A.; Handley, E.R.; Moroney, J.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Somanchi, A.; Handley, E.R.; Moroney, J.V. submitted to the EMBL Data Library, March 1998
A;Description: Identification of a cyclophllin cDNA from Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Molecule type: mRNA
A;Residues: 1-172 <SOM>
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A; Accession: T07950
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Best Local :
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Best Local Similarity 100.0%; Pred. No. 7.5e-06;
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126 TAWLDGKHVVFGKV 139
                                                                                                                                85 FHRVIKDFMIQGGD 98
                                                                                                       9
                                                                                                                                                                                                                                  Local Similarity
                                                                                                    FHRVIKDFMIQGGD
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                                                                                                    102
                                                                                                                                                                                                    Score 14; DB 2; Le
; Pred. No. 9e-06;
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EMBL; M60457; AAA35733.1; -
PIR; A39118; CSHUB.
PIR; A40515; A40515.
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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SWISS-2DPAGE; P23284; HUMAN.
ABrhus/Ghent-2DPAGE; 117; NE
Genew; HGNC:9255; PPIB.
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01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
(Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1).
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FUNCTION: PPIases accelerate the folding of proteins.
the cis-trans isomerization of proline imidic peptide
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SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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              CYPB_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=92096454; PubMed=1756174; Schumacher A., Schroeter H., Multhaup G., Nordheim A.; Schumacher A., Schroeter H., Multhaup G., Nordheim A.; Murine cyclophilin-51: a variant peptidyl-prolyl isomerase with a putative signal sequence expressed in differentiating F9 cells."; Biochim. Biophys. Acta 1129:13-22(1991).

-I- FUNCTION: PPIases accelerate the folding of proteins. It cataly the cis-trans isomerization of proline imidic peptide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:97750; Ppib.
Interpro; IPRO02130; CSA_PPIase.
Interpro; oro_isomerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91260697; PubMed-1710767;
Hasel K.W., Glass J.R., Godbout M., Sutcliffe J
"An endoplasmic reticulum-specific cyclophilin.
Mol. Cell. Biol. 11:3484-3491(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-91260697;
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M60456; AAA37498.1; -.
EMBL; X58990; CAA41736.1; -.
PIR; B39722; B39722.
PJR; S21835; S21835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                 Multigene
                                                                                                                                                                                                                                                                                                                                                                              Cyclosporin; Isomerase;
                                                                                                                                                                   54
                                                                                                                                                                                 ENZYME RÉGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By simi
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligopeptides.
CATALYTIC ACTIVITY:
                                                                                                       RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT
                                                                                                                                    RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 151
                                                                                                                                                                   FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P23284; 1CYN
                                                                                                                                                                                                                             Similarity 100
)8; Conservative
                                                                                                                                                                                                                                                                                                                                                                family.
                                                                                                                                                                                                                                                                                         208 AA;
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                               STANDARD;
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                                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                                             Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                    PEPTIDYL-PROLYL CIS-TRANS
PREVENT SECRETION FROM ER
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                         4B8DF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Signal; Endoplasmic reticulum;
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Matches 77
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Bose S., Muecke M., Freedman R.B.;
Pho Characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase from the endoplasmic-reticulum lumen.";
cis-trans-isomerase from the endoplasmic-reticulum lumen.";
Biochem. J. 300:871-875(1994).
-i--FUNCTION: PPIases accelerate the folding of proteins. I
                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
PROSITE; PS50072; CSA_PPIASE_2; Signal; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carrello A., Mark P.J.,
Submitted (JAN-1993) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Uterus;
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15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B precursor (EC (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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  143
                                              143 QFFITTVKTAWLDGKHV 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                             SKFHRVIKDFMIOGGDFTRGDGTGGKSIYGERFDDENFKLKHYGDGWVSMANAGKDTNGS
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QFFITTVKTAWLDGKHV
                                                                                     SKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGS
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                                                                                                                                                                                                l Similarity
77; Conserv
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208 AA;
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Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                               37.0%;
159
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                                                                                                                                                                                           Score 77; DB; Pred. No. 1.9
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PREVENT SECRETION FROM ER
K -> G (IN REF. 3).
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1.9e-63;
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CHAIN
                                                                                     CYPB_CHICK
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-!- FUNCTION: Phrases accelerate the folding of proteins.

-the cis-trans isomerization of proline imidic peptide oligopeptides.

-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92112948; PubMed=1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B precursor (EC (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclosporin;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene
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PROSITE; PS50072; CSA_PPIASE_2; 1.
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ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By

SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FA
                                                                                                                                                                                                           VKT 151
                                                                                                                                                                                                                                                                                              IKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITT
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199
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; 76D12AC3427FEF32 CRC64;
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PEPTIDYL-PROLYL CIS-TRANS
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P24367; 01-MAR-1992 (Rel. 2 01-MAR-1992 (Rel. 2 15-JUN-2002 (Rel. 4

21, Created)
21, Last sequence up
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STANDARD;

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Best Local S
Matches 55
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence upda
01-FEB-1995 (Rel. 41, Last annotation up
15-JUN-2002 (Rel. 41, Last annotation up
Peptidyl-prolyl cis trans isomerase (EC
(Cyclophilin homolog).
Streptomyces chrysomailus.
Batteria; Actinobacteria; Actinobacteria
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PPI_STRCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caroni P., Rothenfluh A., McGlynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-91250364; PubMed-2040593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50772; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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   SEQUENCE FROM N.A. STRAIN-ATCC 11523; MEDLINE-93116593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M63553; AAA49064.1; -. PIR; A40516; A40516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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CATALYTIC ACTIVITY: Peptidylproline (omega-180)
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                                                                                                                                                                    Streptomycineae;
      PubMed-1474897
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                                                                      SEQUENCE
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ycineae; Streptomycetaceae;
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PEPTIDYL-PROLYL
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(EC 5.2.1.8)
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3.1e-4
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family
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                                                                                                                                                                                                                                                                                                   (PPIase)
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Best Local 9
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pahl A., Uehlein M., Bang H., Schlumbohm W., Keller U.;
"Streptomycetes possess peptidy1-prolyl cis-trans isomerases
strongly resemble cyclophilins from eukaryotic organisms.";
MOI. Microbiol. 6:3551-358(1992).
-1- FUNCTION: pplases accelerate the folding of proteins. It
the cis-trans isomerization of proline imidic peptide bon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYP5_CA
P52013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130: CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS0072; CSA_PPIASE_2; 1.
CYclospor1n; Isomerase; ROtamase,
CYclospor1n; Isomerase; ROtamase,
CYCLOSPORTN; ISOMERASE,
SEQUENCE 165 AA; 17716 MW; 2CF1DF725CD6F47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-Bristol N2;

MEDLINE-96276416; PubMcd-8694762;

Page A.P., Macniven K., Hengartner M.O.;

Page A.B., Macniven K., Hengartner M.O.;

"Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peptidyl-prolyl cis-trans isomerase 5
(Cyclophilin-5).
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                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematc
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P05092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z15137; CAA78840.1; -.
This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo
                                                                                                                        -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
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ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATE:
OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline (omega=180) =
                                                                                                                                                                         FUNCTION: PPIases accelerate the the cis-trans isomerization of pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S28020; S28020.
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1 Similarity 100.0%;
19; Conservative
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                                                                                                                          Peptidylproline
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Pred. No.
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(EC 5.2.1.
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                          is produced through
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                                                                                                                          (omega=180)
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imidic peptide
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                                                                                                                             peptidylproline
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                                                                                                                                                                                                                                                        elegans.";
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          a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: PPIAses accelerate the folding of proteins.
the cis-trans isomerization of proline imidic peptide oligopeptides.
-- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline (omega=180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p52014;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase 6 precursor
                                                                        EMBL; U27354; AAC47124.1;
EMBL; U00051; AAA91355.1;
HSSP; P23284; ICYN.
                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-96276416; PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page A.P., Macriven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegablochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rotamase) (Cyclophilin-6).
CYP-6 OR F42G9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Multigene family.
SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          WormPep; F42G9.2; CE01301.
InterPro; IPR002130; CSA_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute. The by non-profit institutions as long
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17; Conser
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  pro_isomerase;
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CSA_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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hes 0;
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                                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                          Usage
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                                                                                                     EMBL;
EMBL;
HSSP;
                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institutions as long as its content is used by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-94304830; PubMed-8031755;

Schneider H., Charara N., Schmitz R., Weh
Zurini M.G., Quesniaux V.F., Movva N.R.;

"Human cyclophilin C: primary structure,
determination of binding specificity for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peptidyl-prolyl cis-trans isomerase C
(Cyclophilin C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYPC_HUMAN P45877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases -1- FUNCTION: PPTases accelerate the folding of proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00153; CSAPPISMRASE. PROSITE; PS00170; CSA_PPIASE_1; PR0SITE; PS50072; CSA_PPIASE_2;
                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 33:8218-8224(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPIC OR CYPC.
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                      ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC. SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                         the cis-trans isomerization of proline imidic peptide bonds in oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
                                                                                                                                                                                                                                                                                                   (omega=0).
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                                                                                                  S71018; AAB31350.1; -. BC002678; AAH02678.1; P05092; 2RMC.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE N-LINKED (GLCNAC. . .) (POTENTIAL). , 084C5762917F958B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wehrli S., Mikol V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
(EC 5.2.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
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2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclosporins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue distribution,
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InterPro; IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.

Rotamase; Multigene

Genew;

HGNC:9256; PPIC

123842;

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CYPC_MCM

CYPC_MC

P30412

DC P40412

DC P40412

OC EUKATY

OC EUKATY

OC MAMMMAL

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OC EUKATY

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OC HAMMMAL

OC -1- FUL

CC -1- FUL

CC -1- SIL

CC -1-
RESULT 11
CYP7_CAEEL
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Best Local S
Matches 16
                                                                                                                                                                                            Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                    Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPISWRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Cyclosporin; Isomerase; Rotamase; Multigene family.
SEQUENCE 212 AA; 22794 MW; C99E7AA5DOFA04B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P05092; 2RMC.

MGD; MGI:97751; Pplc.

InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          affinity for a new cyclophilin: absence of CsA."; Cell 66:799-806(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase) (Rotamase)
(Cyclophilin C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-91347379; PubMed-1652374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M74227; AAA37511.1; -. PIR; A40047; A40047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Two cytoplasmic candidates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYPC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                 87
                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PPIases accelerate the folding the cis-trans isomerization of proline in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKFHRVIKDFMIQGGD 98
                                                                                                                                               FHRVIKDFMIQGGDFT 100
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                                                                                               FHRVIKDEMIQGGDET
                                                                                                                                                                                                 Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
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                                                                                                                                                                                                                     100.0%;
                                                                                                 102
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6F3DB547A2AE581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunophilin action
one in the presence
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                     DB 1;
2.2e-(
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                                                                                                                                                                                                                     .2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ng of proteins. It catalyzes imidic peptide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        revealed by one in the
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p52015;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Rotamase)
                                                                                                                         CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-97295299; PubMed-9150941;
Bini L., Held H., Liberatori S., Geler G., Pallini V., Zwilling R.;
"Two-dimensional gel electrophoresis of Caenorhabditis elegans
homogenates and identification of protein spots by microsequencing.";
Electrophoresis 18:557-562(1997).
-i- FUNCTION: PDTASES accelerate the folding of proteins. It catalyzes
the cis-trans isomerization of proline imidic peptide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptidyl-prolyl cis-trans (Cyclophilin-7). CYP-7 OR Y75B12B.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYP7_CAEEL
                                                                                                                                                                        PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                 EMBL; U27559; AAC47125.1; -. EMBL; AL032663; CAA21760.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegationem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
MEDLINE-96276416; PubMed-8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - 1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                         Isomerase; Rotamase; Multigene family.
CONFLICT 12 12 I -> T (IN REF. 1).
SEQUENCE 171 AA; 18401 MW; D5BD5E32A32942A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Bristol N2;
 123
                                148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligopeptides.
CATALYTIC ACTIVITY:
TVKTAWLDGKHVVFG
                              TVKTAWLDGKHVVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s:
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematoda; Chromadorea; rinae; Caenorhabditis.
 137
                                162
                                                                             100.
                                                                                             7.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidylproline (omega=180) -
                                                                            .08;
                                                             0;
                                                                                         Score 15;
                                                                            Pred.
                                                               Mismatches
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                                                             1.5e-06;
hes 0;
                                                                                             DB 1;
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                                                                                          Length 171;
                                                                                                                            CRC64;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidylproline
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RESULT 12 CYPB_CAEEL

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RESULT
PPIB_TR
ID
ID
AC
OC
DT
115
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Best Loc
Matches
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O66105
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01-CCT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase 11 (EC 5.2.1.8) (PPlase)
(Rotamase) (Cyclophilin-11).
CYP-11 OR 701B7.4.
                                                                          (Rotamase).
PPIB OR PPI OR TP0947.
       Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                     TREPA
                                                                                                                                                                                                                                                                                                                               PPIB_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Multigene family.
SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U34955; AAC47115.1;
EMBL; Z66499; CAA91297.1;
HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2; MEDLINE=96276416; PubMed=8694762;
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CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
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15; Conser
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Eukaryota; Vir Spermatophyta;

Viridiplantae; Str yta; Magnoliophyta;

Streptophyta;

eptophyta; Embryophyta; Tracheophyta, Liliopsida; Asparagales; Alliaceae;

Allium cepa

(Onion).

01 FEB-1994 (Rel. 28, Created)
01 FEB-1994 (Rel. 28, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peptidyl-prolyl cis-trans isomerase (f
(Cyclophilin) (Cyclosporin A-binding)

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CYPH_ALLCE RESULT

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                                                                                                                                                              Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                   Isomerase;
SEQUENCE
                                                                                                                                                                                                                                                        HSSP; P05092; 2RMC.
TIGR; TP0947; -
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EMBL; AE001263; AAC65904.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of homologs for thioredoxin, peptidyl prolyl cis-trans isomerase, and glycerophosphodiester phosphodiesterase in outer membrane fractions from Treponema pallidum, the syphilis spirochete."; infect. Immun. 65:4179-4189(1997).
                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Radolf J.D.;
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68
                              85 FHRVIKDFMIQGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PPIASES accelerate the folding of proteins. the cis-trans isomerization of proline imidic peptide oligopeptides (By similarity).

CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptides (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBD outstation - Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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FHRV1KDFM1QGGD
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23272 MW; CCA1589C1F5A6D0B CRC64;
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-i- FUNCTION: PPIAses accelerate the folding of proteins.
the cls-trans isomerization of proline imidic peptide oligopeptides.
-i- CATALYTIC ACTIVITY: Peptidylproline (omega=180) - pep
STRAIN-S288c / AB972;

MEDLINE-94378003; Pubbed-8091229;

MEDLINE-94378003; Pubbed-8091229;

Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,

Kucaba T., Hiller L., Jier M., Johnston L., Langston Y.,

Kucaba T., Hiller L., Macri C., Mardis E., Menezes S., Mouser L.,

Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,

Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P23285;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seguence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidy1-proly1 cls-trans isomerase B precursor
(Rotnmase) (Cyclophilin B) (Cyclophilin-related
CPR2 OR CYP2 OR SCC2 OR CRG OR YHR057C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90221907; PubMed-2183199;
Koser P., Sylvester D., Livi G.P., Bergsma D.J.;
"A second cyclophilin-related gene in Saccharomy
Nucleic Acids Res. 18:1643-1643(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
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Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
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Pfam; PF00160; pro_isomerase; 1.
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HSSP; P05092;
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13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Isomerase; Rotamase; Multigene family.
150 AA; 16033 MW; 9223D16840F7E241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA32642.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
9.6e-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 5.2.1.8) (PPIase) protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It catalyzes bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Search completed: April 10, Job time : 12 secs

2003, 11:54:34

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밁
                                                                     Query Match
Best Local
                                                         Matches
                                                                                                                                                                      HSSP; P23284; 1CYN.

SGD; S0001099; CYP2.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS500772; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porter T.G., Levy M.A., Livi G.P.:
"The CYP2 gene of Saccharomyces cerevisiae enc
sensitive peptidyl-prolyl cis-trans isomerase
signal sequence.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koser P., Bergsma D.J., Cafferkey Ferrara A., Silverman C., Kasyan K Porter T.G. 15000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence VIII.";
                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                         EMBL; x51497; CAA35865.1; ALT_SEQ.
EMBL; U00061; AAB68386.1; -.
PIR; S12324; S12324.
PIR; S46707; S46707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 108:73-80(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                               CHAIN
                                                                                                                                              Cyclosporin; Isomerase; SIGNAL 1 20
                                                                                                                   SEQUENCE
 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligopeptides
GKDTNGSQFFITT
                            GKDTNGSQFFITT 148
                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long
                                                                                                                 21
205 AA;
                                                                                                                 205 I
22769 MW;
 149
                                                                    6.2%;
100.0%;
                                                                                                                 ROTAMASE; Signal; Multigene family.
ROTENTIAL).
POPTENTIAL).
PEPTIDYL-PROLYL CIS-TRANS ISON
69 MW; 616EAEB434837A6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidylproline (omega=180)
                                                           0;
                                                                       Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of.
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae chromosome
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'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bossard M.J., Johnson R.K.,
                                                                        DB 1; L
0.00012;
                                                                                                                                                                                                                                                                                                                                                                                               as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encodes a cyclosporin A-
ase with an N-terminal
                                                                                                                   CIS-TRANS ISOMERASE A6D CRC64;
                                                                                    Length 205

    peptidylproline

                                                            0
                                                           Gaps
                                                            0
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